

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 25, 2004, 02:27:18 ; Search time 85 Seconds  
(without alignments)  
4839.873 Million cell updates/sec

Title: NP000123

Perfect score: 7803

Sequence: 1 MQIELSTCFPLCLLRCFSA.....WVHQIALRMEVLCGEAQDLY 1456

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Geneseq19808:\*

2: Geneseq19908:\*

3: Geneseq20008:\*

4: Geneseq20018:\*

5: Geneseq20028:\*

6: Geneseq20038:\*

7: Geneseq20038s:\*

8: Geneseq20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7619.5	97.6	1661	2 AAW18670	AAW18670 Factor VII
2	7577.5	97.1	1471	4 AAB67959	Aab67959 Amino aci
3	7565.5	97.0	1471	2 AAW23414	Aaw23414 Human B-d
4	7535.5	96.6	1459	4 AAE10832	Aae10832 Human fac
5	7525.5	96.4	1459	4 AAE10833	Aae10833 Human fac
6	7522.5	96.4	1459	4 AAE10827	Aae10827 Human fac
7	7520.5	96.4	1457	2 AAW46246	Aaw46246 Human fac
8	7520.5	96.4	1457	2 AAW44372	Aaw44372 Human fac
9	7510.5	96.3	1447	5 ABG92541	Abg92541 5Arg B-do
10	7508.5	96.2	1457	2 AAY21675	Aay21675 Beta-doma
11	7501.5	96.1	1445	5 ABG32540	Abg32540 LE B-doma
12	7412.5	95.0	1424	4 AAB48842	Aab48842 Mutant ma
13	7412.5	95.0	1424	5 AAO18622	Aao18622 Human mat
14	7407.5	94.9	1438	3 AAB01262	Aab01262 B-domain
15	7401.5	94.9	1425	1 AAP80267	Aap80267 Modified
16	7398.5	94.8	1424	1 AAP80268	Aap80268 Modified
17	7394.5	94.8	1424	1 AAP91169	Aap91169 Sequence
18	7392	94.7	1440	2 AAR12971	Aar12971 Factor VI
19	7362	94.3	1516	1 AAP80265	Aap80265 Modified
20	7340	94.1	2342	2 AAW11422	Aaw11422 Active Fa
21	7339	94.1	2344	2 AAW11432	Aaw11432 Active Fa
22	7338.5	94.0	2345	2 AAW11453	Aaw11453 Active Fa
23	7338.5	94.0	2345	2 AAW11441	Aaw11441 Active Fa
24	7338.5	94.0	2345	2 AAW11446	Aaw11446 Active Fa
25	7338	94.0	2346	2 AAW11434	Aaw11434 Active Fa

26	7338	94.0	2346	2 AAW11421	AAW11421 Active Fa
27	7338	94.0	2346	2 AAW11452	AAW11452 Active Fa
28	7338	94.0	2346	2 AAW11431	AAW11431 Active Fa
29	7337	94.0	2348	2 AAW11436	AAW11436 Active Fa
30	7337	94.0	2348	2 AAW11449	AAW11449 Active Fa
31	7337	94.0	2348	2 AAW11448	AAW11448 Active Fa
32	7337	94.0	2348	2 AAW11444	AAW11444 Active Fa
33	7336.5	94.0	2349	2 AAW11420	AAW11420 Active Fa
34	7336.5	94.0	2349	2 AAW11440	AAW11440 Active Fa
35	7336.5	94.0	2349	2 AAW11424	AAW11424 Active Fa
36	7336.5	94.0	2349	2 AAW11428	AAW11428 Active Fa
37	7336.5	94.0	2349	2 AAW11430	AAW11430 Active Fa
38	7336.5	94.0	2349	2 AAW11443	AAW11443 Active Fa
39	7335.5	94.0	2351	1 AAP50059	Aap50059 Human fac
40	7335.5	94.0	2351	2 AAW11427	AAW11427 Active Fa
41	7335.5	94.0	2351	2 AAW11445	AAW11445 Active Fa
42	7335.5	94.0	2351	2 AAW11425	AAW11425 Active Fa
43	7335.5	94.0	2351	2 AAW11437	AAW11437 Active Fa
44	7335.5	94.0	2351	2 AAW11329	AAW11329 Native Fa
45	7335.5	94.0	2351	2 AAW11435	AAW11435 Active Fa

## ALIGNMENTS

### RESULT 1

AAW18670

ID AAW18670 standard; protein; 1661 AA.

XX AAW18670;

XX 10-AUG-1997 (first entry)

XX Factor VIII-dB695-HCII.

XX Factor VIII-dB695-HCII.

XX Factor VIII-dB695-HCII; heparin cofactor II; blood coagulation;

KW blood clotting; procoagulant; anticoagulant; antithrombotic; haemophilia;

XX gene therapy.

XX Homo sapiens.

XX Key

XX Domain

XX Location/Qualifiers

XX 731..760

XX /label= HCII

XX /note= "heparin cofactor II acidic domain"

XX WO9718315-A1.

XX 22-MAY-1997.

XX 13-NOV-1996; 96WO-EP004977.

XX 13-NOV-1995; 95US-00558107.

XX (IMMO ) IMMUNO AG.

XX Voorberg JJ;

XX WPI; 1997-289291/26.

XX N-PSDB; AAT69811.

XX Hybrid Factor VII with modified activity, comprises region from donor

XX anticoagulant or antithrombotic protein - useful for treatment of

XX coagulation disorders.

XX Claim 11; Page 52-60; 96pp; English.

XX Factor VIII-dB695-HCII (AAW18670) is a hybrid protein in which amino

XX acids 712-736 of Factor-dB695 (Factor VII del868-1562) B-domain are

XX replaced by amino acids 51-80 from the acidic region (and potential

XX thrombin-binding site) of human heparin cofactor II (HCII). It is the

XX expression product of Factor VIII-dB695-HCII DNA (AAT69811) in plasmid

XX pCLB-dB695-HCII. The hybrid protein, which can be expressed using gene

CC therapy techniques, has increased procoagulant activity owing to the HCII  
 CC acidic region, and can be used to treat blood coagulation disorders such  
 CC as haemophilia A  
 XX  
 SQ Sequence 1661 AA;

Query Match	97.6%	Score 7619.5;	DB 2;	Length 1661;
Best Local Similarity	87.2%	Pred. No. 0;		
Matches 1449;	Conservative 2;	Mismatches 5;	Indels 205;	Gaps 4;
QY	1	MQIELSTCFCLLRFCSATRRYYLGAVELSWDMQSDLGELPVDARFPFRVPKSPFFN	60	
DB	1	MEIELSTCFCLLRFCSATRRYYLGAVELSWDMQSDLGELPVDARFPFRVPKSPFFN	60	
QY	61	TSVVYKKTFLVEFTDHLFNIAKPPPPWMLGGLPTIQAEVDTVTITLKNMASHPVSLHAV	120	
DB	61	TSVVYKKTFLVEFTDHLFNIAKPPPPWMLGGLPTIQAEVDTVTITLKNMASHPVSLHAV	120	
QY	121	GVSTWKASGEAEYDDQTSQREKDDKVPFGSHTYVMQVLKENGPMASDPLCLTYSYLH	180	
DB	121	GVSYWKASGEAEYDDQTSQREKDDKVPFGSHTYVMQVLKENGPMASDPLCLTYSYLH	180	
QY	181	VDLVKDLNSGLIGALLVCREGLAKETQTLHKETILLFAVDECKSHSETKNSLMQDRD	240	
DB	181	VDLVKDLNSGLIGALLVCREGLAKETQTLHKETILLFAVDECKSHSETKNSLMQDRD	240	
QY	241	AASARAWPKMHTVNGYNRSLPGLIGCHRKSVYWHVIGMTTPEVHSIFLEGHTFLVRNH	300	
DB	241	AASARAWPKMHTVNGYNRSLPGLIGCHRKSVYWHVIGMTTPEVHSIFLEGHTFLVRNH	300	
QY	301	ROASLEISPIFTLTAQTLMDLQGLFLFCHISSHQHDMGEAYKVDSCEPEPQLRMKNE	360	
DB	301	ROASLEISPIFTLTAQTLMDLQGLFLFCHISSHQHDMGEAYKVDSCEPEPQLRMKNE	360	
QY	361	EAEDYDDDLTSEMDVVRFDNDNSPSFIQIRSVAKHPKTVWHVIAAEBEDWDYAPLVLA	420	
DB	361	EAEDYDDDLTSEMDVVRFDNDNSPSFIQIRSVAKHPKTVWHVIAAEBEDWDYAPLVLA	420	
QY	421	PDRSRYKSOYLNNQPGRIQKRYKVRFWAYTDEFKTRAIQHESGILGPLLXGEVGDTL	480	
DB	421	PDRSRYKSOYLNNQPGRIQKRYKVRFWAYTDEFKTRAIQHESGILGPLLXGEVGDTL	480	
QY	481	LIIPKNOASRPYNIYPHGIITDVRPLYSRRLPKGVKHLKDPFIPLGEIFYKWTVTEDGP	540	
DB	481	LIIPKNOASRPYNIYPHGIITDVRPLYSRRLPKGVKHLKDPFIPLGEIFYKWTVTEDGP	540	
QY	541	TKSDPRCLTRYSSFYVNERDLASGLIGPLLI CYKESVDORGQINSDKNVILFSVFE	600	
DB	541	TKSDPRCLTRYSSFYVNERDLASGLIGPLLI CYKESVDORGQINSDKNVILFSVFE	600	
QY	601	NRSWYLTENIORPLNPAGVQLEDPEFOASNIHNSINGYVFDLSQLSVCLHEVAYWYILS	660	
DB	601	NRSWYLTENIORPLNPAGVQLEDPEFOASNIHNSINGYVFDLSQLSVCLHEVAYWYILS	660	
QY	661	IGAQTDFLSVFFSGYTFKHKVWYEDTLTLPFFSGETVFMGMENPGLMWILGCHNSDFNRG	720	
DB	661	IGAQTDFLSVFFSGYTFKHKVWYEDTLTLPFFSGETVFMGMENPGLMWILGCHNSDFNRG	720	
QY	721	MTALLKUSSC---DKNTGDI-----YED-----SFSQNSRHSTKQKQF	756	
DB	721	MTALLKUSSCIPGEEDDDYLDLEKIFSEDDYDIDVDSLIEPRSPFSQNSRHSTKQKQF	780	
QY	757	NATTIPENDIEKTDWFAHRTMPKIQNVSSDMLMLL-----	794	
DB	781	NATTIPENDIEKTDWFAHRTMPKIQNVSSDMLMLLROSPTPHGLSUSDLQEAKEYTF	840	
QY	795	-----	794	
DB	841	SDDPSCAIDSNNSLSBTHFRPQLHSGDMVFTPESSGLQLRLNEKLGTTADPLANDNH	900	
QY	795	-----	794	
DB	901	GTOIPKEWKSQEKSPKTAFFKDKDTLSLNACESNHATAAINEGONKPEIEVTWAKQGR	960	

QY	795	-----EMKKEDFDIYDDENQSPRSF	815	
DB	961	TERLCSQNPVLKRHOREITRRTLQSDQBEIDYDDTISVEMKKEDFDIYDDENQSPRSF	1020	
QY	816	QKTRHYFIAAVERLWDYGMSSSPHVLNRNRAQSGSVPOFKKVVQFQFTDGSFTQPLVRGE	875	
DB	1021	QKTRHYFIAAVERLWDYGMSSSPHVLNRNRAQSGSVPOFKKVVQFQFTDGSFTQPLVRGE	1080	
QY	876	LNHGLGLGPYRAEVEDNIMVTFRNQAQSRPSYFSSLSISYBEDQROGAEPKXNFVKPNE	935	
DB	1081	LNHGLGLGPYRAEVEDNIMVTFRNQAQSRPSYFSSLSISYBEDQROGAEPKXNFVKPNE	1140	
QY	936	TKTYFWKVOHHMPTKDEFCKAWAYPSVDVLEKOVHSLIGPLLYCHNTNLNPAHGRQV	995	
DB	1141	TKTYFWKVOHHMPTKDEFCKAWAYPSVDVLEKOVHSLIGPLLYCHNTNLNPAHGRQV	1200	
QY	996	TVOEPALFTTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYFAHNGYIMDTLPG	1055	
DB	1201	TVOEPALFTTIFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYFAHNGYIMDTLPG	1260	
QY	1056	LVMAQDORIRWYLLSGNSNENIHSIHFSCHVTVRKKEEYKMAALYNLYPGVFETVEMLPS	1115	
DB	1261	LVMAQDORIRWYLLSGNSNENIHSIHFSCHVTVRKKEEYKMAALYNLYPGVFETVEMLPS	1320	
QY	1116	KAGIWRVECLIGEHLAGMSTLFLVYSNKCOTPLGMAHGHIRDFQITASGOYQOWAPKLA	1175	
DB	1321	KAGIWRVECLIGEHLAGMSTLFLVYSNKCOTPLGMAHGHIRDFQITASGOYQOWAPKLA	1380	
QY	1176	RLHYSGSINAWSTKEPFSWIKVDLLAPMIHIGIKTGARQKFSLSYISOFIIMYSLDGKK	1235	
DB	1381	RLHYSGSINAWSTKEPFSWIKVDLLAPMIHIGIKTGARQKFSLSYISOFIIMYSLDGKK	1440	
QY	1236	WQTYRGNSTGTLMVFFGNVDSGGIKHNPPIIARYIRLHPTHYSIRSLTLMELMGCDL	1295	
DB	1441	WQTYRGNSTGTLMVFFGNVDSGGIKHNPPIIARYIRLHPTHYSIRSLTLMELMGCDL	1500	
QY	1296	NCSMPLGMEKSAISDAQITASSYFTNMPATWSPSKARLHLOGRSNAMRPQVNNPKWLQ	1355	
DB	1501	NCSMPLGMEKSAISDAQITASSYFTNMPATWSPSKARLHLOGRSNAMRPQVNNPKWLQ	1560	
QY	1356	VDFQTKMKTGVTGTVGKSLTSMYVKBFLISSQDGHOWTLFFQNGKVKVFGNQDSFT	1415	
DB	1561	VDFQTKMKTGVTGTVGKSLTSMYVKBFLISSQDGHOWTLFFQNGKVKVFGNQDSFT	1620	
QY	1416	PVNSLDPLPLTRYIRIHPQSWHQAIALRMEVLGCEAODLY	1456	
DB	1621	PVNSLDPLPLTRYIRIHPQSWHQAIALRMEVLGCEAODLY	1661	

RESULT 2

AAB67959 standard; protein; 1471 AA.

XX AAB67959;

XX AC

XX 29-JUN-2001 (first entry)

XX Amino acid sequence of human B-domain deleted factor VIII.

XX Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;

XX coagulation disorder.

XX Homo sapiens.

XX WO200127303-A1.

XX 19-APR-2001.

XX 12-OCT-2000; 2000WO-US028221.

XX 12-OCT-1999; 99US-0158780P.